

## SEQUENCE LISTING

- <110> Genentech, Inc.  
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- <140> 09/665,350  
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- <150> PCT/US00/04414  
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- <150> US 60/143,048  
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- <150> US 60/145,698  
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- <150> US 60/146,222  
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- <150> PCT/US99/20594  
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- <150> PCT/US99/20944  
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<212> PRT

<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
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Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
                85                      90                      95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
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Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
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Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
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Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
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Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
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<211> 2206

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<213> Homo sapiens

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aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
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<211> 379

<212> PRT

<213> Homo sapiens

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
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His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
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Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
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Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<211> 21

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<213> Artificial Sequence

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<210> 7

<211> 22

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<213> Artificial Sequence

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 <213> Artificial Sequence

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<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35              40              45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50              55              60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65              70              75              80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85              90              95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100             105             110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115             120             125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
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His Asp Pro Gly

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 <223> a, t, c or g

<220>  
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 <223> a, t, c or g

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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<210> 15

<211> 22

<212> DNA

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<210> 16

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<210> 17

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<212> DNA

<213> Homo sapiens

<400> 17

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aatggcagcc tgagcacagc gtaggcctt aataaacacc tgttgataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gcca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggctcgg catggcgccc t 41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
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 ttaccatacg cctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240  
 tatttttatt ccgtacttca gaaatggggc tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaaactt tgtctactgt aatgagcgaa 420  
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 ttctccattt gcaggaaaac aatattcaga ccatctcacg ggctgctctt gccagctct 660  
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 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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aagggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttgggt 1200
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
          20                      25                      30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
          35                      40                      45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
          50                      55                      60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
          65                      70                      75                      80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
          85                      90                      95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
          100                      105                      110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
          115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

<210>	29
<211>	21
<212>	DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggctctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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gaggaagacc	cgggtggctg	cgccctgcc	tgccttccc	ggcgccggcg	gctgcagcct	180
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<210> 34
<211> 915
<212> PRT
<213> Homo sapiens
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<400> 34															
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			20					25					30		
Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu
		35					40					45			
Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser
	50					55					60				
Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile
65					70					75					80
Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val
				85					90					95	
Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys
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His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu
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145					150					155					160
Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
				165					170					175	
Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe
			180					185					190		
Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly
		195					200					205			
Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln
	210					215					220				
Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
305	310	315	320			
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
385	390	395	400			
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
465	470	475	480			
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

### <213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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cggcacctgc aggtccgtgc gtcccgcggc tggcgccct gactccgtcc cggccaggga 120
gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcctgg 180
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ggttgaggc ggtggaggga ggggaagtgg tgcctccagc gtggtacacc ttgcacgggg 300
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ccttgggtcta ctccatgccc tcccgaacc tgtccctgcg gctggagggt ctccaggaga 480
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tttgatatgaa aaa 1813

```

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
 ctgagccgtg ggctgcagtc tcgc 24  
  
 <210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
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 gtgaaatcgc caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtctgtt ggcgaaaatg 240  
 ctaattgcac taacacagaa ggaagtattt attgtatgtg tgtacctggc ttcagatcca 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcc a tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
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 aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660  
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 tatacaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860  
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 agagaatggt ggataattac aactgcacaa aaataaaaaat tccaagctgt ggatgaccaa 2160

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tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtatttttaa 2220
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gttgcccttg aaactagtc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
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aa

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<210> 49
<211> 690
<212> PRT
<213> Homo sapiens

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<400> 49
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1              5              10              15

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100             105             110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115             120             125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130             135             140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145             150             155             160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165             170             175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

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	180		185		190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val	195		200		205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys	210		215		220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe	225		230		235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		245		250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		260		265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		275		280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		290		295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		305		310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile		325		330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		340		345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		355		360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		370		375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		385		390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		405		410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		420		425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		435		440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		450		455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480  
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 485 490 495  
 Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510  
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 Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560  
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 565 570 575  
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 625 630 635 640  
 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655  
 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670  
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685  
 Leu Arg  
 690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (61)

<223> a, t, c or g

<400> 50  
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 gtattggtcc ctttgcttcc atcatctgac aacttcttat tgaaacctca aaattatgat 180  
 aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240  
 ccaccacat tatatgaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300  
 gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360  
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 aatcacctga cacattttgc aattttgatg tctctgggc cttccattgg tattaagat 480  
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcacatg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

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Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20                      25                      30

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His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
    35                      40                      45

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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
    50                      55                      60

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Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
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 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
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 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
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 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
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 Val Arg Ser Pro Ser Phe Glu Lys  
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&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 60

atccgccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

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<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
           35                                  40                                  45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
           50                                  55                                  60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
           65                                  70                                  75                                  80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                                   85                                  90                                  95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                                   100                                  105                                  110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
           115                                  120                                  125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
           130                                  135                                  140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
           145                                  150                                  155                                  160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                                   165                                  170                                  175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                                   180                                  185                                  190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
           195                                  200                                  205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
           210                                  215                                  220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
           225                                  230                                  235                                  240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                                   245                                  250                                  255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
           260                                  265                                  270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
           275                                  280                                  285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
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305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttgtga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgcgata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
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<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
      20                      25                      30

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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
  35                      40                      45

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
  50                      55                      60

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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
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 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

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Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr				
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Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro				
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Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu				
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Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala				
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Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys				
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Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr				
545				550					555					560					
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys				
				565					570					575					
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys				
		580					585						590						
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn				
	595						600					605							
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	610					615					620								

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
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<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
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 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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accgagccga gcggaccgaa ggcgcgcccg agatgcaggt gagcaagagg atgctggcgg 60
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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
                   50                  55                  60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
                   65                  70                  75                  80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
                   85                  90                  95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
                   100                  105                  110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
                   115                  120                  125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
                   130                  135                  140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
                   145                  150                  155                  160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
                   165                  170                  175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
                   180                  185                  190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
                   195                  200                  205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
                   210                  215                  220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
                   225                  230                  235                  240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
                   245                  250                  255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
                   260                  265                  270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
                   275                  280                  285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
                   290                  295                  300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
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 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
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 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
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 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
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 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
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 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
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 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
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 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
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 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
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 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590	
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<210> 75			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
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<210> 76			
<211> 52			
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gg			52
<210> 77			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
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<400> 77  
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<210> 78  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 78  
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<210> 79  
 <211> 50  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<210> 80  
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 <212> DNA  
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<400> 80  
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<210> 81  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 81  
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<210> 82

<211> 50  
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic  
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<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
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 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
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 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
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 210 215 220  
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 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
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Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
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Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
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Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
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His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<400> 85

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22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

<400> 87  
cctagcacag tgacgagggga cttggc 26

<210> 88  
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<212> DNA  
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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 89  
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<212> DNA  
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oligonucleotide probe

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<210> 90  
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<212> DNA  
<213> Homo sapiens

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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr  
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Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe  
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Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn  
65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu  
85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
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 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
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 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660	665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
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Cys Gly Ser His Ser Leu Ser Asp		
690	695	

<210> 92  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 92  
 gttggatctg ggcaacaata ac 22

<210> 93  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 93  
 attgttgatgc aggctgagtt taag 24

<210> 94  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 94  
 ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
 <211> 2226  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
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 tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

gaggggaagg gagggggaac cggggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
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 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

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	355		360		365	
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr						
	370		375		380	
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe						
385		390		395		400
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr						
	405		410		415	
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln						
	420		425		430	
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu						
	435		440		445	
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val						
	450		455		460	
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu						
465		470		475		480
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala						
	485		490			

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20



<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 99  
 acagagcaga gggcgccttg 20  
  
 <210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 100  
 tcagggacaa gtggtgtctc tccc 24  
  
 <210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 101  
 tcagggaagg agtgtgcagt tctg 24  
  
 <210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 102  
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 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

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tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

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&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
          20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
          35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
          50              55              60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

<213> Homo sapiens

<400> 108

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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
  20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
  35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
  50              55              60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
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 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
      370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
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 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcacccccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgcctcccgc gaaagaggtt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcattggagc agcggctgcc gcccacagc gagctggtgc aggcctgtgt 420  
 gcggtctctt caggagccgg tcccccaaggc cgcgtctcac aggcacgggc ggctgtcccc 480  
 ggcagcgcgc cgggccccgg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
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 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660  
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 ggtccgcttt gcctcgagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
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 acctgagggc agaaagcccc ntgtgtcatt gtttacttgt cctgtcactg gatctgggt 1500  
 aaagtccctc accaccactc tggacctaag acctgggggt aagtgtgggt tgtgcatccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45



Glu 50	Glu	Leu	Val	Ile	Pro	Thr 55	His	Val	Arg	Ala	Gln 60	Tyr	Val	Ala	Leu
Leu 65	Gln	Arg	Ser	His	Gly 70	Asp	Arg	Ser	Arg	Gly 75	Lys	Arg	Phe	Ser	Gln 80
Ser	Phe	Arg	Glu	Val 85	Ala	Gly	Arg	Phe	Leu 90	Ala	Leu	Glu	Ala	Ser 95	Thr
His	Leu	Leu	Val 100	Phe	Gly	Met	Glu	Gln 105	Arg	Leu	Pro	Pro	Asn 110	Ser	Glu
Leu	Val	Gln 115	Ala	Val	Leu	Arg	Leu 120	Phe	Gln	Glu	Pro	Val 125	Pro	Lys	Ala
Ala 130	Leu	His	Arg	His	Gly	Arg 135	Leu	Ser	Pro	Arg	Ser 140	Ala	Arg	Ala	Arg
Val 145	Thr	Val	Glu	Trp	Leu 150	Arg	Val	Arg	Asp	Asp 155	Gly	Ser	Asn	Arg	Thr 160
Ser	Leu	Ile	Asp	Ser 165	Arg	Leu	Val	Ser	Val 170	His	Glu	Ser	Gly	Trp 175	Lys
Ala	Phe	Asp	Val 180	Thr	Glu	Ala	Val	Asn 185	Phe	Trp	Gln	Gln	Leu 190	Ser	Arg
Pro	Arg	Gln 195	Pro	Leu	Leu	Leu	Gln 200	Val	Ser	Val	Gln	Arg 205	Glu	His	Leu
Gly 210	Pro	Leu	Ala	Ser	Gly	Ala 215	His	Lys	Leu	Val	Arg 220	Phe	Ala	Ser	Gln
Gly 225	Ala	Pro	Ala	Gly	Leu 230	Gly	Glu	Pro	Gln	Leu 235	Glu	Leu	His	Thr	Leu 240
Asp	Leu	Gly	Asp	Tyr 245	Gly	Ala	Gln	Gly	Asp 250	Cys	Asp	Pro	Glu 255	Ala	Pro
Met	Thr	Glu 260	Gly	Thr	Arg	Cys	Cys	Arg 265	Gln	Glu	Met	Tyr	Ile 270	Asp	Leu
Gln	Gly	Met 275	Lys	Trp	Ala	Glu	Asn 280	Trp	Val	Leu	Glu	Pro 285	Pro	Gly	Phe
Leu 290	Ala	Tyr	Glu	Cys	Val	Gly 295	Thr	Cys	Arg	Gln	Pro 300	Pro	Glu	Ala	Leu
Ala 305	Phe	Lys	Trp	Pro	Phe 310	Leu	Gly	Pro	Arg	Gln 315	Cys	Ile	Ala	Ser	Glu 320
Thr	Asp	Ser	Leu	Pro 325	Met	Ile	Val	Ser	Ile 330	Lys	Glu	Gly	Gly	Arg 335	Thr

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgccca taacttgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagtgtg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggtgtg tgtgtcagtg gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat tggcgatcct gttgtgctcc 120  
 ctggcattgg gcagtgttac agtgcaactct tctgaacctg aagtcagaat tcctgagaat 180

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aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240
tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
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gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
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tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
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ctctgccctg tctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttggt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattttaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaacc tactggaaat acaaagttag ccaggcatgg tgggtgcatg ctgtagctcc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

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<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10              15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
          20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
          85              90              95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
                   100                  105                  110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
                   115                  120                  125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
                   130                  135                  140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145                                  150                  155                  160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
                                   165                  170                  175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
                                   180                  185                  190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
                   195                  200                  205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
                   210                  215                  220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225                                  230                  235                  240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
                                   245                  250                  255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
                                   260                  265                  270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
                   275                  280                  285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
                   290                  295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagt ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120  
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggaact gcagcgatgg cagcgatgag gaggagtgc 300  
ggattgagcc atgtaccag aaagggcaat gccaccgcc cctggcctc ccctgccctc 360  
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgctgcga cggccaccca gactgtccc actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagtg 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtccctc 660  
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggc caccgccacc ctctccttt 780  
tgtcctggct ccgagccag gagcgccctc gccactggg gttactggg gccatgaagg 840  
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900  
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtacct 960  
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccttgagca ctccctatgg agatccgggg 1080  
agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                                     85                                    90                                    95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                                     100                                    105                                    110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                                     115                                    120                                    125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                                     130                                    135                                    140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                                     145                                    150                                    155                                    160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                                     165                                    170                                    175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                                     180                                    185                                    190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                                     195                                    200                                    205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                                     210                                    215                                    220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                                     225                                    230                                    235                                    240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                                     245                                    250                                    255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                                     260                                    265                                    270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                                     275                                    280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
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 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggtttcagc tggcgtgtg cttcgccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360  
 ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaaggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600  
 atgaaggatt caagatccgg taccocgacc tacacaatat ggtttcatta tgcgcgatg 660  
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 acggaactgt ggtggagttt tactgcatc ctggctacag cctcaccagc gactacaagt 1020  
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatacag 1080  
 agcaaacgtg gccagcacc catgagaccc tctgaccac gtggaagatt gtggcggtca 1140



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gcttgagtgc cttaggcccc ggggtacatg cctctgtggg ccagggtgc cccttaccgc 1380
tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttggtcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cttttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1              5              10              15

```

```

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
          20              25              30

```

```

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
    35              40              45

```

```

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
    50              55              60

```

```

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
    65              70              75              80

```

```

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
          85              90              95

```

```

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
    100              105              110

```

```

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
    115              120              125

```

```

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
    130              135              140

```

```

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
    145              150              155              160

```

```

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
          165              170              175

```

```

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

180												185				190			
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr				
		195					200					205							
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys				
		210					215					220							
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu				
225					230					235									
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe				
				245					250					255					
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val				
				260					265					270					
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr				
		275					280					285							
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys				
		290					295					300							
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr				
305					310					315									
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu				
				325					330					335					
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His				
				340					345					350					
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe				
				355					360					365					
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala				
				370					375					380					
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val				
385							390					395							
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr				
				405							410								
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys				
				420							425								
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro				
				435											445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile				
				450											460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg 23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc 23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct 50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gctcccgctg cggcccgctg gtggcctaga 60  
 gatgctgctg ccgcggttgc agttgtgcgc cagcctctg ccgcccagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgc ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240  
 tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtc gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600
gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctctctctcc 900
ttgtgggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
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tccagctcga ccttatgaga aggtaccttg ccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acgacagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<210> 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactg 240  
 cctgcaccag cggcggtggt cctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
 tcctctcaag ccgctccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctgggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggctt ttattcgttc 660  
 cactaacatt tttcggaatc tggagtccac ccgttggttg ctggctgggc ttttccagt 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga gggtgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
          20             25             30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
          35             40             45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
          50             55             60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
          65             70             75             80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
          85             90             95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
          100            105            110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
          115            120            125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
          130            135            140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
          145            150            155            160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
          165            170            175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 143  
 ccaactacca aagctgctgg agcc 24

<210> 144  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 144  
 gcagctctat taccacggga agga 24

<210> 145  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 145  
 tccttcccgt ggtaatagag ctgc 24

<210> 146  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 146  
 ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 ctctctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
 cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
 ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtathtt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtc gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccacaga 480
gagctctttc tccccagtc cagaggggtg caggctggct gacggccctg ggcatcgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaaccctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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athttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgt 1140
ggtagggcatc atctaactct ttgagtgcct gaatagaaga aaaacacaga agaagggagc 1200
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cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga tcttagagga 1560
acggaathtt aaggataaat tttctgaatt gggtatgggg tttctgaaat tggctctata 1620
atctaattag atataaaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149  
ttcagctcat caccttcacc tgcc 24

<210> 150  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150  
ggctcataca aaataccact aggg 24

<210> 151  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151  
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152  
<211> 1427  
<212> DNA  
<213> Homo sapiens

<400> 152  
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctcgacctcg 60  
accacgcgt ccgcggacgc gtggcgagac gcgtgggccc gctaccagga agagtctgcc 120  
gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tggtcggctg 180  
cctgggcgtc ttcggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240  
gaatgctgtg gtggtgatca caggcgccac ctccagggtg ggcaaagaat gtgcaaaagt 300  
cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360  
gctcatcaga gaacttaccg cttctcatgc caccaagggt cagacacaca agccttactt 420  
ggtgaccttc gacctcacag actctggggc catagtgcga gcagcagctg agatcctgca 480  
gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600  
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660  
catcagcagc atccagggca agatgagcat tccctttcga tcagcatatg cagcctccaa 720  
gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780  
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccacaccgcg 840  
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900  
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
cttactgcct tccttggtg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgccgcc atggcccaac ttgtttattg cagcttataa tgggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1                      5                      10                      15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
                20                      25                      30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
                35                      40                      45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
  50                      55                      60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
  65                      70                      75                      80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
                85                      90                      95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
                100                      105                      110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
                115                      120                      125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
  130                      135                      140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
  145                      150                      155                      160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
                165                      170                      175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
                180                      185                      190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
                195                      200                      205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

20

<400> 156  
tcatactgtt ccatctcggc acgc

24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatgggtgggg ccctagaaga gctcatcaga gaactcacg cttctcatgc

50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacaccaaa cgctcgcagc caaaaagggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aaggggactgg gtgccaaagg 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420  
gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaaca catgtctgtg tcctaatttc gtaaactctg gcttcatcaa 780  
aaatccaagt acaagtttgg gaccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccatttct tcaatatcat ttttgaggct ttggcagtct 1140  
tcatttacta ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta ttttgattg cacttaaatt ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtggtatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctacccatt 1500  
gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta ccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

<400> 159

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
130 135 140

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145					150					155					160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
245 250 255



Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
                   260                  265                  270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
                   275                  280                  285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
                   290                  295                  300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180  
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctcgccc tttcccagga 300  
 ctgaacatga agagtatatgc cggcttcctc accgtgaata agacttacia cagcaacctc 360  
 ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
 caggggtggc cgggaggttc atccatgttt ggactctttg tggacatgg gccttatgtt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttccctt ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660  
 atatttctctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840  
 tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900  
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggttga ggcctttgaa 960  
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020  
 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080  
 tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140  
 tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200  
 ccatgggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
 atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320  
 caggaatata agaaggcaga aaaaaaagtt tggaaagatct ttaaactctga cagtgaagtg 1380  
 gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440  
 attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500  
 aaaggatggg atccttatgt tggataaaact accttcccaa aagagaacat cagaggtttt 1560  
 cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620  
 tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
 ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740  
 ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
 ttttagggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tcttttctg ccaataacag aagtttggca tgccgtgaag 1920  
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980  
 ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150				155						160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
		180						185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
	275						280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgccca cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 167  
 agctctcaga ggctggatcat aggg

24

<210> 168  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 168  
 gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169  
 <211> 2477  
 <212> DNA  
 <213> Homo sapiens

<400> 169  
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 atttttccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120  
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180  
 tccttgccctc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240  
 gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300  
 cctggagagc ctgggggagg gcctgcctaa caagctttca aaaaacagga ggcacttcca 360  
 ctgggctggg ataagacgtg ccggtaggat aggggaagact ggggttagtc ctaatatcaa 420  
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480  
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540  
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tccaaagagg 600  
 gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
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 tgggtgctgc tggccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020  
 ggggccatca accgggtcta taagctgaca ggcaacctga ccatccagggt ggctcataag 1080  
 acagggccag aagaggacaa caagtctcgt taccgcgcc tcacgtgca gccctgcagc 1140  
 gaagtgtc caatgtcaac aagctgctca tcattgacta ctctgagaac 1200  
 cgcctgctgg cctgtgggag cctctaccag ggggtctgca agctgctgcg gctggatgac 1260  
 ctcttcaccc tgggtggagc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320  
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 ggcacggctg tggatgggaa gcaggattac ttcccgaccc tgtccagccg gaagctgccc 1440  
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 ctcatcaaga tcccttcaga caccctggcc ctggtctccc actttgacat cttctacatc 1560  
 tacggctttg ctagtggggg ctttgtctac tttctcactg tccagccoga gacccctgag 1620  
 ggtgtggcca tcaactccgc tggagacctc ttctacacct cagcctcgt gcggctctgc 1680

```

aaggatgacc ccaagttcca ctcatacgtg tccctgcctt tcggctgcac ccgggccggg 1740
gtggaataacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgctt gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980
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tgtggactgg acatcaacca gccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
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aggggttaat tttgtgactt agcttctagc tacttctctc agccatcagt cattgggtat 2400
gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1             5             10             15

```

```

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
          20             25             30

```

```

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
          35             40             45

```

```

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
          50             55             60

```

```

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
          65             70             75             80

```

```

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
          85             90             95

```

```

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
          100            105            110

```

```

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
          115            120            125

```

```

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
          130            135            140

```

```

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
          145            150            155            160

```

```

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
          165            170            175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctcccgc gcgcggctga gtgcggactg gagggtggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctgggtccctc 180  
tgccggctccg ccacgcacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggccctc 480  
acatctgcag tgagatggac ctccggggct tgcccagctg gctactccaa gaccctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat ttgaccacc 600  
tgatgtccag ggtggtgcc ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagaaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tcttgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccaggga gtcttgcca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac cacccttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900  
actggacggg gtggtttgac tegtggggag gccctcacia tatcttgat tcttctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggctcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtacg 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttccggctca tctcaggcat ccctctccct ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
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tgccagtc aa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
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tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccagcg caaaggctta atttgaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttcttca gaggttcggc ctggacaaat 1680  
ggngttccct ccagaaaca ccacattac ctgcttctt cttgggtagc ttgtccatca 1740  
gtccacgcc ttgtgacacc tttctgaagc tggagggctg ggagaagggg gtgtattca 1800  
tcaatggcca gaaccttgga cgttactgga acattggacc ccagaagacg cttacctcc 1860  
caggtccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc acctgggcag gaaccagta attaatgtag 1980  
cgggtggcacc ccctcctgct ggtgccagt ggagactgcc gctcctctt gacctgaagc 2040  
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggt 2160  
ggatggctct gggcctggct ttgttgatga tggcttccct acagccctgc tcttggcgg 2220  
aggctgtcgg gctgtctcta ggggtgggag agctaatac atcgcccagc ctttggccct 2280

```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctgctg 2340
gactcaggcg tgcctcttgc tggttcctgg gaggcttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
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cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctcctc 3000
gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taacctgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1              5              10              15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20              25              30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
          35              40              45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
          50              55              60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
          65              70              75              80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85              90              95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
          100             105             110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
          115             120             125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
          130             135             140

```



Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
 ccctggtgag gggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120  
 aaggggagca aagccgggct cgccccgagg cccccaggac ctccatctcc caatgttggg 180  
 ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgcgt gtaaacgcca 240  
 tggctcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300  
 tgctgccccca ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360  
 tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

```

tgcctttgggc cgaccggcctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg ctcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
aggtcttgct gcccagata tatccatggc tttatcacaa tgggggcaac atcattagca 780
ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
ctgacaacat gacccaaatc tttaccctgc ttcggaagta tgaacccat gggccattgg 1020
taaactctga gtaactacaca ggctggctgg attactgggg ccagaatcac tccacacggt 1080
ctgtgtcagc tgtaaccaa ggactagaga acatgctcaa gttgggagcc agtggtgaaca 1140
tgtacatgtt ccattggagg accaactttg gatattggaa tgggtgccgat aagaaggagc 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatactctgaa gcaggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320
gacctttacc tccccgagc cccaagatga tgcttgacc tgtgactctg cacctggttg 1380
ggcatttact ggctttccta gacttgcttt gcccccgctg gccattcat tcaatcttgc 1440
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cccataccat ttttgagcca acaccattct ggggtgcaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatag agagacaaac 1620
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tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
ggtttccctt ccagtgtcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
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ggccacaaca gacctctac gtgccaaagt tcctgctgtt tcctagggga gccctcaaca 2040
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tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
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ggagaattgc ttgaatccag gaggcagagg ttgcagtga tggaggttgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

```

&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10              15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20              25              30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35              40              45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50              55              60

```

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

	340		345		350										
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro
	355						360					365			
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu
	370					375					380				
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu
385					390					395					400
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr
				405					410					415	
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val
			420					425					430		
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val
	435						440					445			
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr
	450					455					460				
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg
465					470					475					480
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro
				485					490					495	
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu
			500					505					510		
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys
		515					520					525			
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr
	530					535					540				
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly
545					550					555					560
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr
				565					570					575	
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu
			580					585					590		
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu
		595					600					605			
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu
	610					615					620				

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625                                      630                                      635                                      640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
                                     645                                      650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22



<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
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 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420  
 tgcactgtgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcaattgaga tgcccttcac tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctaagaaaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcagatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact ggaacaaaag tggacattct gccaaaacaa ttgtttaaat 1320

```

gcataaaagt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
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agggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgcttgctaa agtaaattgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaaa 1947

```

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1              5              10              15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20              25              30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35              40              45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50              55              60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65              70              75              80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85              90              95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100              105              110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115              120              125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130              135              140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145              150              155              160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
      165              170              175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
      180              185              190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                                      470                                      475                                      480  
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro  
    485                                      490                                      495  
 Phe Ala Asn Gly Ile  
    500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
    oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c                                      21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
    oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg                                      24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
    oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag                                      47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 cccacgcgtc cggccttctc tctggacttt gcattttccat tccttttcat tgacaaactg 60  
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccctggg 120  
 aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcaattatct gcctaggtac atcgaagtct tttagacctc atacagtgat tatgcctgtc 300  
 atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcctttac 360  
 ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420  
 cacaaccag acaaggtgtg gtgggccaa aacagccagg ccaaaaccat tgccacggag 480  
 tcttgtcctg coctgcagt ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
 cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780  
 ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tgggtcctta aggctgccc a ggccttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020  
 gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080  
 aatatggcag agaccacaaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
 tggacaatat aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320  
 tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
 gtcttctact acttcttctc tcttaacatc tctattccaa actgtggcgg ttacctggat 1440  
 accttggag gatccttcac cagccccaat tacccaaagc cgcacctga gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaaact caaagagatt 1560  
 ttcctagaaa tagacaaaaca gtgc aaattt gattttcttg ccatctatga tggccctctc 1620  
 accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacct cgaatcgtca 1680  
 tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
 gcttctaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgtcttct 1800  
 gacaggatga gagttattat aagcaaatcc tactagagg cttttaactc taatgggaat 1860  
 aacttgcaac taaaagacc aacttgca ccaaaattat caaatgttgt ggaattttct 1920  
 gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
 aatataatca ccttttctgc atcctcaact tctgaagtga tcaccctga gaaacaactc 2040  
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
 gaagatgatg taatacaaa tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
 tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
 caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggt ggtgttctt 2280  
 gatacctgta gagcctctcc cacctctgac ttgtcatctc caacctacga cctaatacaag 2340  
 agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
 ttccagttta atgcctttta attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
 gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaagggtg tgtctccaga 2520  
 agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
 ctgaaaagg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgaggaa 2640  
 gaaactccaa accagccttt caacagtgtg catctgtttt ccttcatggg tctagctctg 2700  
 aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggcctgaaag tgacacacag gcctgcatgt aaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
			580					585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
			595				600					605			

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gtcctccagg ctgcggttcc cgttgctgct gttgctgttg 120  
 ctgctgctgc cgccgcgcgc gtgcctgcc cacagcgcca cgcgcttcga cccacactgg 180



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gagtcacctgg acgccccgcca gctgccccgcg tggtttgacc aggccaaagtt cggcatcttc 240
atccactggg gagtggttttc cgtgcccagc ttcggtagcg agtgggttctg gtgggtattgg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattacc tcttagtttc 360
aaatatgaag attttggacc actattttaca gcaaaatttt ttaatgcaa ccagtgggca 420
gatatttttc aggcctctgg tgccaaatac attgtcttaa ctccaaaca tcatgaaggc 480
tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccag 540
agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttgg 600
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ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtatgc 840
accaatgata gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gaggaagct ggaatctctg actatcttac aattgaagaa 1020
ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttcat gaatattggg 1080
cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtggggtcc 1140
tggtctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
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gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380
aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
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atgtctaagg ctaggaaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
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cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcactactt aatatgggga tttttctgg gaaatgcatt gctagtcaat 1860
ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacacctaata gtgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtggt tatttgtata tcgaaacata tggaaacata 2040
gagaaggtag agtaaaaata ctgtaaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgtct tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgaacttta 2280
caaacgtttt aattttttaa acottttttg ctcttttgta ataacttta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

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&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
  1                      5                      10                     15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
                20                      25                     30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
  35                      40                     45

```

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
                   340                  345                  350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
                   355                  360                  365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
                   370                  375                  380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
                   385                  390                  395                  400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
                   405                  410                  415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
                   420                  425                  430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                  440                  445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
                   450                  455                  460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttgacgc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgcc agcttcggta gcgagtgggt ctgggtgggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaaa tccggatgtc tccggttatga agtggagcag tgagtgtgag cctcaacata 60  
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 catctgaggt gtttcctcgg ctctgaagggt gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcaattccat ctggaccacg aggtccttg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccagggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtggtcatc tctaggatta gcccaaaccc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccacaaa 600  
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gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
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```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35              40              45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50              55              60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65              70              75              80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100              105              110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115              120              125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130              135              140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 203  
 gtcagtgcaca gtacctactc gg 22

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 204  
 tggagcagga ggagtagtag tagg 24

<210> 205  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 205  
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206  
 <211> 1620  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (973)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (977)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (996)  
 <223> a, t, c or g

<220>  
 <221> modified\_base

<222> (1003)

<223> a, t, c or g

<400> 206

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ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
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ccaacacaat tcttttcttc cgcttggata ttcgcatggg cctactttac atcacactct 360
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acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80



Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagtggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 tggggcccca gcctggccc ggtcaccctg gcatgaggag atgggacctgt tgctcctggt 120  
 cccattgctc ctgctgccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
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 aggggcccctc aggtgtgtgt actttggaca ataaatgggt ctatgactgc cttccgcca 1860  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125
Val Ser Leu Glu Ile Gln Asp	Leu Arg Leu Glu Asp	Tyr Gly Arg Tyr
130	135	140
Arg Cys Glu Val Ile Asp	Gly Leu Glu Asp	Glu Ser Gly Leu Val Glu
145	150	155
160		
Leu Glu Leu Arg Gly Val Val Phe	Pro Tyr Gln Ser Pro Asn Gly Arg	
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly	Gln Gln Val Cys Ala Glu Gln Ala	
180	185	190
Ala Val Val Ala Ser Phe Glu Gln	Leu Phe Arg Ala Trp Glu Glu Gly	
195	200	205
Leu Asp Trp Cys Asn Ala Gly	Trp Leu Gln Asp Ala Thr Val Gln Tyr	
210	215	220
Pro Ile Met Leu Pro Arg Gln	Pro Cys Gly Gly Pro Gly Leu Ala Pro	
225	230	235
240		
Gly Val Arg Ser Tyr Gly	Pro Arg His Arg Arg Leu His Arg Tyr Asp	
245	250	255
Val Phe Cys Phe Ala Thr Ala	Leu Lys Gly Arg Val Tyr Tyr Leu Glu	
260	265	270
His Pro Glu Lys Leu Thr Leu Thr	Glu Ala Arg Glu Ala Cys Gln Glu	
275	280	285
Asp Asp Ala Thr Ile Ala Lys	Val Gly Gln Leu Phe Ala Ala Trp Lys	
290	295	300
Phe His Gly Leu Asp Arg Cys	Asp Ala Gly Trp Leu Ala Asp Gly Ser	
305	310	315
320		
Val Arg Tyr Pro Val Val His	Pro His Pro Asn Cys Gly Pro Pro Glu	
325	330	335
Pro Gly Val Arg Ser Phe Gly	Phe Pro Asp Pro Gln Ser Arg Leu Tyr	
340	345	350
Gly Val Tyr Cys Tyr Arg Gln	His	
355	360	

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttggtg gggtggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagtgc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgcg gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc ttgcccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 tggccagggg aggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180  
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
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 gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
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 ggaggacctg gacagaaaca aagatggcta tgtccagggt gaggagtaca tcgcggatct 720  
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 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
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 gggcggcggg cgcgggtgag agggatccct gacgcctctg tccctgttcc tttgtcgctc 120  
 ccagcctgtc tgcctcgatt tggcgcccc cgcctccccg cgggtgcgggg ttgcacaccg 180  
 atcctgggct tcgctcgatt tgccgcagag ggcctccca gacctagagg ggcgtggcc 240  
 tggagcagcg ggctgctctg gtccctctct ctctgcgccg cggccgggga tccgaagggt 300  
 gcggggctct gaggaggatga cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccgctc 420  
 tcggcctcgg tgtgtgtctg ctgctgctgc cggggccccg gggcagcgag ggagccgctc 480  
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 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
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 tccagtctca aatgctttct agatggtctg cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
 tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140  
 agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccaaaag 1200  
 tgggtggtgg atttattgat ggttggcctt ctgatgacat cgaggaagca ggcattgttg 1260  
 ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320  
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 toctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860  
 cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920  
 tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gagttcacag 1980  
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040  
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 attgtattct cataatactg aaatgcttta gcatactaga atcagataca aaactattaa 2160  
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<210> 227

<211> 550  
 <212> PRT  
 <213> Homo sapiens

<400> 227

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Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
 1           5           10           15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
      20           25           30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
      85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
      100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
      115          120          125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
      130          135          140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
      145          150          155          160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
      165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
      180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
      195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
      210          215          220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
      225          230          235          240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
      245          250          255

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Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
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 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttccctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga ttcc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
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 gtcggggcg ggcgtgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gcctgctgct ggcgggcgcg gtccccacgg ccccgcgcc cgtccgacg gcgacctcgg 240  
 ctccagtcaa gcccgggccg gctctcagct accgcagga ggaggccacc ctcaatgaga 300  
 tggtccgcga gggtgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
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 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcg 600  
 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

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gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
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aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2586
aaaaaa

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&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

```

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
  1             5             10             15

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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
          20             25             30

```

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
          35             40             45

```

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Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
          50             55             60

```

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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
          65             70             75             80

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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                     85                                    90                                    95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                     100                                    105                                    110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                     115                                    120                                    125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                     130                                    135                                    140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                     145                                    150                                    155                                    160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                     165                                    170                                    175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                     180                                    185                                    190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                     195                                    200                                    205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
                     210                                    215                                    220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                     225                                    230                                    235                                    240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                     245                                    250                                    255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                     260                                    265                                    270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
                     275                                    280                                    285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                     290                                    295                                    300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
                     305                                    310                                    315                                    320  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
                     325                                    330                                    335  
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
                     340                                    345                                    350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 237  
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 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
 gcagagcgga gatgcagcgg ctg 24  
  
 <210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
 ttggcagctt catggagg 18  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
 cctgggcaaa aatgcaac 18



<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgagc gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
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 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacataca 150  
 cacacataca ccttctcttc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250  
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 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gactgcaccg ctgcactcca 550  
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ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650  
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 tatacgcccc gctcgtccta ccgcgagget accactgtgg actgcaatga 1050  
 cctattcctg acggcagtcc ccccggcact ccccgcaggc acacagacct 1100  
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 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggctg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350  
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 ccaacctcct gagggccatt gacagccgtt ggtttgaaat gctgcccac 1450  
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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
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Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
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Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
				110					115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
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Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	155	160	165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
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Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
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Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
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Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
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				425					430					435					
Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His	Cys	Arg	Ala	Leu	Ala	Glu					
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Pro	Glu	Pro	Glu	Ile	Tyr	Trp	Val	Thr	Pro	Ala	Gly	Leu	Arg	Leu					
				455					460					465					
Thr	Pro	Ala	His	Ala	Gly	Arg	Arg	Tyr	Arg	Val	Tyr	Pro	Glu	Gly					
				470					475					480					
Thr	Leu	Glu	Leu	Arg	Arg	Val	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Tyr					
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Thr	Cys	Val	Ala	Gln	Asn	Leu	Val	Gly	Ala	Asp	Thr	Lys	Thr	Val					
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Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu	Gln	Pro	Gly	Arg	Asp	Glu					
				515					520					525					
Gly	Gln	Gly	Leu	Glu	Leu	Arg	Val	Gln	Glu	Thr	His	Pro	Tyr	His					
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Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr	His	Ser	Tyr	Asn	Ile	Thr					
				575					580					585					
Arg	Leu	Leu	Gln	Ala	Thr	Glu	Tyr	Trp	Ala	Cys	Leu	Gln	Val	Ala					
				590					595					600					
Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala	Cys	Val	Trp	Ala	Arg	Thr					
				605					610					615					
Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala	Leu	Gly	Asp	Arg	Pro	Gly					
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Leu	Ile	Ala	Ile	Leu	Ala	Leu	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly					
				635					640					645					
Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln	Pro	Arg	Lys	Gly	Val	Gly					
				650					655					660					
Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp	Ala	Phe	Trp	Gly	Trp	Ser					
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Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                                 680                                685                                690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
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Leu Pro Pro Leu Ser Gln Asn Ser  
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgatcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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				20					25					30

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40					45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55					60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70					75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85					90

Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu	125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp	140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu	155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp	170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val	185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu	200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala	215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp	230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu	245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr	260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu	275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp	290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr	305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr	320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser	335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn	350	355	360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
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Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
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Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
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Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
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Ala	Asp	Lys	Glu	Gln	Ala									
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&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

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&lt;210&gt; 252

&lt;211&gt; 24

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<210> 253  
 <211> 47  
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 <223> Synthetic Oligonucleotide Probe

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<210> 254  
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 <212> DNA  
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20				25					30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35				40					45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	80	85	90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	125	130	135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg  
 1 5 10 15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser  
 20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
 50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
 65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
 80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser	95	100	105
Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe	110	115	120
Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro	125	130	135
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr	140	145	150
Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe	155	160	165
Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys	170	175	180
Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln	185	190	195
Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys	200	205	210
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly	215	220	225
Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly	230	235	240
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val	245	250	255
Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val	260	265	270
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met	275	280	285
Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu	290	295	300
Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val	305	310	

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
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Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
				20				25					30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
				35				40					45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50				55					60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65				70					75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
				80				85					90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95				100					105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110				115					120	



Ser Gly Lys Ser	Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile	Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val	Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His	Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val	Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe	Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro	Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val	Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys	Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly	Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn	Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly	Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn	Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp	Cys Arg Glu Gly	380		

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
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 ccatgggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggaccca ccaactgcga ggttctctgc tcaccagccg 300  
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggtcccaga aggtgggtgt tgctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctgggtgcgt ctcgagcgct 500  
 ccatacagtt ctgagagcgg gtctgccc tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac ccaactgctg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650  
 ttctatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750  
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
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 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950  
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000  
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100  
 aataggctca tctacctcta cctctggggg ccggaaggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200  
 catcaggccc cgcccaacgg cctcatgtcc ccgccccccac gacttcgggc 1250  
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300  
 ataggtattt gtaaccctgc ccacatatct tattttattcc tccaatttca 1350  
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
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Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
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<400> 267  
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268  
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<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 268  
ggggaattca ccctatgaca ttgcc 25

<210> 269  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 269  
gaatgccctg caagcatcaa ctgg 24

<210> 270  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
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<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
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<220>  
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<400> 274  
ggcgaagagc aggtgagac cccg 24

<210> 275  
<211> 45

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<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276  
<211> 21  
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<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
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<400> 277  
ggctatgaca gcagggttc 18

<210> 278  
<211> 18  
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<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgcatc gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcagac gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100



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 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu					
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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp					
			20						25					30					
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala					
			35						40					45					
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp					
			50						55					60					
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val					
			65						70					75					
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe					
			80						85					90					
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu					
			95						100					105					
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys					
			110						115					120					
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala					
			125						130					135					

Lys Thr Glu Arg	Ile Gly Cys Gly Ser	His Phe Cys Glu Lys Leu
140	145	150
Gln Gly Val Glu	Glu Thr Asn Ile Glu	Leu Leu Val Cys Asn Tyr
155	160	165
Glu Pro Pro Gly	Asn Val Lys Gly Lys	Arg Pro Tyr Gln Glu Gly
170	175	180
Thr Pro Cys Ser	Gln Cys Pro Ser Gly	Tyr His Cys Lys Asn Ser
185	190	195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu	Asp Ala Gln Asp Leu Pro
200	205	210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe	Arg Ala Thr Glu Ala Ser
215	220	225
Asp Ser Arg Lys	Met Gly Thr Pro Ser	Ser Leu Ala Thr Gly Ile
230	235	240
Pro Ala Phe Leu	Val Thr Glu Val Ser	Gly Ser Leu Ala Thr Lys
245	250	255
Ala Leu Pro Ala	Val Glu Thr Gln Ala	Pro Thr Ser Leu Ala Thr
260	265	270
Lys Asp Pro Pro	Ser Met Ala Thr Glu	Ala Pro Pro Cys Val Thr
275	280	285
Thr Glu Val Pro	Ser Ile Leu Ala Ala	His Ser Leu Pro Ser Leu
290	295	300
Asp Glu Glu Pro	Val Thr Phe Pro Lys	Ser Thr His Val Pro Ile
305	310	315
Pro Lys Ser Ala	Asp Lys Val Thr Asp	Lys Thr Lys Val Pro Ser
320	325	330
Arg Ser Pro Glu	Asn Ser Leu Asp Pro	Lys Met Ser Leu Thr Gly
335	340	345
Ala Arg Glu Leu	Leu Pro His Ala Gln	Glu Glu Ala Glu Ala Glu
350	355	360
Ala Glu Leu Pro	Pro Ser Ser Glu Val	Leu Ala Ser Val Phe Pro
365	370	375
Ala Gln Asp Lys	Pro Gly Glu Leu Gln	Ala Thr Leu Asp His Thr
380	385	390
Gly His Thr Ser	Ser Lys Ser Leu Pro	Asn Phe Pro Asn Thr Ser
395	400	405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
                   410                                  415                                  420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
                   425                                  430                                  435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
                   440                                  445                                  450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
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<210> 286  
 <211> 19  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 286  
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<210> 287  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 287  
 ctcatattgc acaccagtaa ttcg 24

<210> 288  
 <211> 45  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 288  
 atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289  
 <211> 3662  
 <212> DNA  
 <213> Homo Sapien

<400> 289  
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 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
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Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20				25					30	

Ala Ser Ser Met	Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu	35	40	45
Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser		50	55	60
Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu		65	70	75
Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu		80	85	90
Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro		95	100	105
Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr		110	115	120
Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu		125	130	135
Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys		140	145	150
Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn		155	160	165
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala		170	175	180
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		185	190	195
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		200	205	210
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		215	220	225
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		230	235	240
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		245	250	255
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		260	265	270
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		275	280	285
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser				



290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile 305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg 320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala 335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys 380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly 410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp 425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala 440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser 455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu 470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln 485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu 500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn 515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn 530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg 545	550	555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560		565	570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575		580	585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
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Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
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Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620		625	630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635		640	645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650		655	660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665		670	675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680		685	690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695		700	705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710		715	720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725		730	735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740		745	750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755		760	765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770		775	780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785		790	795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800		805	810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser	815	820	825
Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr	830	835	840
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr	845	850	855
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr	860	865	870
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His	875	880	885
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr	890	895	900
Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His	905	910	915
Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp	920	925	930
Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn	935	940	945
Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu	950	955	960
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn	965	970	975
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu	980	985	990
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg	995	1000	1005
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly	1010	1015	1020
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn	1025	1030	1035
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro	1040	1045	1050
Asn Phe Gln Ser Tyr Asp Leu Asp Thr	1055		

<210> 291  
 <211> 2906

<213> Homo Sapien

1000-251

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

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Tyr	Ala	Phe	Asn	Arg	Ile	Pro	Ser	Leu	Arg	Arg	Arg	Leu	Asp	Leu	Gly		
170										175				180			
Glu	Leu	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly			
185										190				195			
Leu	Ser	Asn	Leu	Arg	Tyr	Leu	Asn	Leu	Ala	Met	Cys	Asn	Leu	Arg			
200										205				210			
Glu	Ile	Pro	Asn	Leu	Thr	Pro	Leu	Ile	Lys	Leu	Asp	Glu	Leu	Asp			
215										220				225			
Leu	Ser	Gly	Asn	His	Leu	Ser	Ala	Ile	Arg	Pro	Gly	Ser	Phe	Gln			
230										235				240			
Gly	Leu	Met	His	Leu	Gln	Lys	Leu	Trp	Met	Ile	Gln	Ser	Gln	Ile			
245										250				255			
Gln	Val	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Asn	Leu	Gln	Ser	Leu	Val			
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Glu	Ile	Asn	Leu	Ala	His	Asn	Asn	Leu	Thr	Leu	Leu	Pro	His	Asp			
275										280				285			
Leu	Phe	Thr	Pro	Leu	His	His	Leu	Glu	Arg	Ile	His	Leu	His	His			
290										295				300			
Asn	Pro	Trp	Asn	Cys	Asn	Cys	Asp	Ile	Leu	Trp	Leu	Ser	Trp	Trp			
305										310				315			
Ile	Lys	Asp	Met	Ala	Pro	Ser	Asn	Thr	Ala	Cys	Cys	Ala	Arg	Cys			
320										325				330			
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Gln	Asn	Tyr	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	Val	Glu	Pro	Pro			
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Ala	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	Leu	Lys	Cys			
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Arg	Ala	Ser	Thr	Ser	Leu	Thr	Ser	Val	Ser	Trp	Ile	Thr	Pro	Asn			
380										385				390			
Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val			
395										400				405			
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp			
410										415				420			

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 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
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 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
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 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
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 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
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 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
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<210> 293

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<212> DNA

<213> Homo Sapien

<400> 293

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<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly	20	25	30	
Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg	35	40	45	
Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys	50	55	60	
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp	65	70	75	
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys	80	85	90	
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	95	100	105	
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	110	115	120	
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	125	130	135	
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	140	145	150	
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	155	160	165	
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	170	175	180	
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	185	190	195	
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	200	205	210	
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Leu Lys Ser Leu Lys Met Gln Arg Asn	Gly Val Thr Lys Leu Met	
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Asp Gly Ala Phe Trp Gly Leu Ser Asn	Met Glu Ile Leu Gln Leu	
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr	Lys Gly Trp Leu Tyr Gly	
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu	Ser Gln Asn Ala Ile Asn	
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe	Cys Gln Lys Leu Ser Glu	
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser	Arg Leu Asp Asp Ser Ser	
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr	Leu His Ile Gly Asn Asn	
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala	Phe Arg Gly Leu Ser Ser	
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn	Glu Ile Ser Trp Thr Ile	
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly	Leu Asp Lys Leu Arg Arg	
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Leu Ile Leu Gln Gly Asn Arg Ile Arg	Ser Ile Thr Lys Lys Ala	
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His	Leu Asp Leu Ser Asp Asn	
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Ala Ile Met Ser Leu Gln Gly Asn Ala	Phe Ser Gln Met Lys Lys	
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser	Ser Leu Leu Cys Asp Cys	
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Gln Leu Lys Trp Leu Pro Gln Trp Val	Ala Glu Asn Asn Phe Gln	
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His	Pro Gln Leu Leu Lys Gly	
470	475	480

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Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	500	505	510
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	515	520	525
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	530	535	540
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	545	550	555
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	560	565	570
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	575	580	585
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	590	595	600
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	605	610	615
Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro	620	625	630
Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro	635	640	645
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val	650	655	660
Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser	665	670	675
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr	680	685	690
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp	695	700	705
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala	710	715	720
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser	725	730	735
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln	740	745	750

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 770 775 780  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
 785 790 795  
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
 800 805 810  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
 815 820 825  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
 830 835 840  
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 860 865 870  
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 875 880 885  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 890 895 900  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 905 910 915  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 950 955 960  
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 965 970 975  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 980 985 990  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 995 1000 1005  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

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Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

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&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe



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<223> Synthetic oligonucleotide probe

<400> 307

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<400> 308

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<210> 309

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<212> DNA

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<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

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<223> Synthetic Oligonucleotide Probe

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<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<210> 313

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<211> 3003

<212> DNA

<213> Homo Sapien

<400> 314

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<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

Thr Cys Val Asp Val Asp Glu Cys Ala	Thr Gly Arg Ala Ser Cys	
170	175	180
Pro Arg Phe Arg Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys	
185	190	195
Lys Cys His Lys Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr	
200	205	210
Gln Cys His Asp Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys	
215	220	225
Ser Ser Phe Ala Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys	
230	235	240
Lys Cys Lys Glu Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr	
245	250	255
Ile Pro Lys Val Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro	
260	265	270
Lys Gly Asn Gly Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn	
275	280	285
Trp Ile Pro Asp Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro	
290	295	300
Tyr Ile Pro Pro Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr	
305	310	315
Thr Arg Pro Thr Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro	
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Pro Pro Pro Leu Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr	
335	340	345
Thr Pro Glu Arg Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala	
350	355	360
Ala Ser Thr Pro Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln	
365	370	375
Thr Asp Pro Gln Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val	
380	385	390
His Ser Cys Asn Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu	
395	400	405
Lys Asp Asn Asp Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly	
410	415	420
Gly Gln Tyr Leu Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys	

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggacccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

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&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

<213> Homo Sapien

<400> 319

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<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu			

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro	Leu Ala Ser Ile Thr	Gly
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met	Cys Leu Leu Phe Leu	Trp
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile	Lys Gln Lys Leu Glu	Gly
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala	Gln Thr Phe Ser Gly	His
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile	Tyr Glu Phe Val Ala	Phe
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile	Pro Ser Arg Ser Val	Pro
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp	Leu His Ser Thr Val	Tyr
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln	Gln Gln Asp His Pro	Glu
440	445	450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatcctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly  
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln  
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

2397  
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2397

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230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu	Glu Ala Glu Ser Lys Glu	
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn	Ala Ile Arg Gln Arg Ser	
260	265	270
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275	280	

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

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&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

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&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

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&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 329

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<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

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<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

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cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val	1	5	10	15
Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met	20	25	30	
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys	35	40	45	
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser	50	55	60	
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75	
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90	
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105	
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120	
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135	
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150	
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165	
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180	
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195	
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210	

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
 485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
 500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
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Pro Cys Gly Ser Thr Glu Val Asp  
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcaciaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe



<400> 336

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<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

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<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
			20						25					30
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35						40					45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50						55					60
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65						70					75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80						85					90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala

	95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val	110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr	125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser	140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg	155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile	170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu	185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala	200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly	215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg	230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro	245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly	260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu	275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu	290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr	305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr	320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val	335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu	350	355	360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
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 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
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 Gln Glu Gln Ala Asn Ser Thr  
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<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
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 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

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<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

&lt;400&gt; 341

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Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				

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His	Ile	Phe	Asn	Asp	Ala	Leu	Val	Phe	Leu	Pro	Pro	Asn	Gly	Ser
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tgtttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200

atttctcagt gcctgtttca tcaccagatg tgttgtagaca tttcgcatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350

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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	
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Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	
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Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	
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Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	
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Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	
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Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	
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Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	
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Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	
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Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	
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Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	
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Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	
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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
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Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
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<400> 417

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gggactgaac tgccagcttc 20

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 <223> Synthetic oligonucleotide probe

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Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu  
35 40 45  
Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr  
50 55 60  
Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr  
65 70 75  
Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly  
80 85 90  
Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val  
95 100 105  
Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg  
110 115 120  
Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val  
125 130 135  
Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val  
140 145 150  
Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly  
155 160 165  
His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu  
170 175 180  
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe  
185 190 195